



1	cgagaaaaggtgacgcggggcccgggcaggcgccggcgccggccccccccccccccgc	
61	cctggttatttggccgccttcgcccgcagctcagggcagagtctcctggaaggcgaggc	
121	agtgtggcgagaagggcgccctgcttggctttcttttctgtctgctttccccggttgccg	
181	ctggaagctgcgcgcgagttcctgcaaggcggtctgcccggccggggccccggccttctc	
241	ccctcgacagcagccccgcctcgccggcgccggccccgaggtagcccaggcgccggag	
301	gagccagccccagcagcgccgggagaggcgccagcgcagccggacgcacagcgacgg	
361	gccggcaccagctcgccggggccgggactcggaactcgccggccggcgccggcgccgg	
421	cccagcgcagggtggggggcgccggggcgccggg	
457	cgccggcgagcggggggccATGCAGGCGCGCTACTCCGTGTCCAGCCCCAACTCC	12
METGlnAlaArgTyrSerValSerSerProAsnSer	
511	CTGGGAGTGGTGCCCTACCTCGCGCGGAGCAGAGCTACTACCGCGCGGCGGCC	30
	LeuGlyValValProTyrLeuGlyGlyGluGlnSerTyrTyrArgAlaAlaAla	
565	GCGGCGGCGCGGGGCGGCTACACCGCCATGCCGCGCCCCATGAGCGTGTACTCG	48
	AlaAlaAlaGlyGlyGlyTyrThrAlaMETProAlaProMETSerValTyrSer	
619	CACCCTGCGCACGCCGAGCAGTACCCGGGCGGCATGGCCCGCGCCTACGGGCCC	66
	HisProAlaHisAlaGluGlnTyrProGlyGlyMETAlaArgAlaTyrGlyPro	
673	TACACGCGCAGCCGAGCCCAAGGACATGGTGAAGCCGCCCTATAGCTACATC	84
	TyrThrProGlnProGlnProLysAspMETValLysProProTyrSerTyrIle	
727	GCGCTCATCACCATGGCCATCCAGAACGCCCGGACAAGAAGATCACCTGAAC	102
	AlaLeuIleThrMETAlaIleGlnAsnAlaProAspLysLysIleThrLeuAsn	
781	GGCATCTACCAGTTCATCATGGACCGCTTCCCCTTCTACCGGGACAACAAGCAG	120
	GlyIleTyrGlnPheIleMETAspArgPheProPheTyrArgAspAsnLysGln	
835	GGCTGGCAGAACAGCATCCGCCACAACCTCTCGCTCAACGAGTGCTTCGTCAAG	138
	GlyTrpGlnAsnSerIleArgHisAsnLeuSerLeuAsnGluCysPheValLys	
889	GTGCCGCGCGACGACAAGAAGCCGGGCAAGGGCAGCTACTGGACGCTGGACCCG	156
	ValProArgAspAspLysLysProGlyLysGlySerTyrTrpThrLeuAspPro	
943	GACTCCTACAACATGTTTCGAGAACGGCAGCTTCCTGCGGCGGCGGCGGCGCTTC	174
	AspSerTryAsnMETPheGluAsnGlySerPheLeuArgArgArgArgPhe	
997	AAGAAGAAGGACGCGGTGAAGGACAAGGAGGAGAAGGACAGGCTGCACCTCAAG	192
	LysLysLysAspAlaValLysAspLysGluGluLysAspArgLeuHisLeuLys	
1051	GAGCCGCCCCCGCCGCGCCAGCCCCCGCCGCGCCGCGGAGCAGGCGGAC	210
	GluProProProProGlyArgGlnProProProAlaProProGluGlnAlaAsp	
1105	GGCAACGCGCCCGGTCCGCGAGCCGCGCCCGTGGCGCATCCAGGACATCAAGACC	228
	GlyAsnAlaProGlyProGlnProProProValArgIleGlnAspIleLysThr	
1159	GAGAACGGTACGTGCCCTCGCCGCCCCAGCCCCGTGCCCCGGCCGCGCCCTG	246
	GluAsnGlyThrCysProSerProProGlnProLeuSerProAlaAlaAlaLeu	
1213	GGCAGCGGCAGCGCCGCGGTCGCCAAGATCGAGAGCCCCGACAGCAGCAGC	264
	GlySerGlySerAlaAlaAlaValProLysIleGluSerProAspSerSerSer	
1267	AGCAGCCTGTCCAGCGGGAGCAGCCCCCGGGCAGCCTGCCGTGGCGCGGGCCG	282
	SerSerLeuSerSerGlySerSerProProGlySerLeuProSerAlaArgPro	
1321	CTCAGCCTGGACGGTGCGGATTCCGCGCCGCGCCCGCCCGCCCTCCGCCCCG	300
	LeuSerLeuAspGlyAlaAspSerAlaProProProAlaProSerAlaPro	
1375	CCGCCGCACCATAGCCAGGGCTTCAGCGTGGACAACATCATGACGTCGCTGCGG	318
	ProProHisHisSerGlnGlyPheSerValAspAsnIleMETThrSerLeuArg	
1429	GGGTGCGCGCAGAGCGCGGCGGAGCTCAGCTCCGGCCTTCTGGCCTCGGCG	336
	GlySerProGlnSerAlaAlaAlaGluLeuSerSerGlyLeuLeuAlaSerAla	
1483	GCCGCGTCTCGCGCGGGGATCGCACCCCCGCTGGCGCTCGGCGCCTACTCG	354
	AlaAlaSerSerArgAlaGlyIleAlaProProLeuAlaLeuGlyAlaTyrSer	
1537	CCCGGCCAGAGCTCCCTCTACAGCTCCCCCTGCAGCCAGACCTCCAGCGCGGGC	372
	ProGlyGlnSerSerLeuTyrSerSerProCysSerGlnThrSerSerAlaGly	

Fig. 1A

1591	AGCTCGGGCGCGCGCGCGCGCGCGCGGGGCCCGCGGGGGCGCGGGCGCGCC SerSerGlyGlyGlyGlyGlyGlyAlaGlyAlaAlaGlyGlyAlaGlyGlyAla	390
1645	GGGACCTACCACTGCAACCTGCAAGCCATGAGCCTGTACGCGGCCGCGAGCGC GlyThrTyrHisCysAsnLeuGlnAlaMETSerLeuTyrAlaAlaGlyGluArg	408
1699	GGGGCCCACTTGCAAGGCGCGCCCGGGGGCGCGGGCGGCTCGGCCGTGGACAAC GlyGlyHisLeuGlnGlyAlaProGlyGlyAlaGlyGlySerAlaValAspAsn	426
1753	CCCCTGCCCCACTACTCTCTGCCTCCGGTCACCAGCAGCAGCTCGTCTCCCTG ProLeuProAspTyrSerLeuProProValThrSerSerSerSerSerSerLeu	444
1807	AGTCACGGCGGCGCGCGCGCGCGCGGGGAGGCCAGGAGGCCGCCACCAC SerHisGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlnGluAlaGlyHisHis	462
1861	CCTGCGGCCACCAAGGCCGCTCACCTCGTGGTACCTGAACCAGCGGGCGGA ProAlaAlaHisGlnGlyArgLeuThrSerTrpTyrLeuAsnGlnAlaGlyGly	480
1915	GACCTGGGCCACTTGGCAAGCGCGCGCGCGGGCGGGCGCGCAGGCTACCCG AspLeuGlyHisLeuAlaSerAlaAlaAlaAlaAlaAlaAlaGlyTyrPro	498
1969	GGCCAGCAGCAGAACTTCCACTCGGTGCGGGAGATGTTTCGAGTCACAGAGGATC GlyGlnGlnGlnAsnPheHisSerValArgGluMETPheGluSerGlnArgIle	516
2023	GGCTTGAACAACCTCTCCAGTGAACGGGAATAGTAGCTGTCAAATGGCTTCCCT GlyLeuAsnAsnSerProValAsnGlyAsnSerSerCysGlnMETAlaPhePro	534
2077	TCCAGCCAGTCTCTGTACCGCACGTCCGGAGCTTTTCGTCTACGACTGTAGCAAG SerSerGlnSerLeuTyrArgThrSerGlyAlaPheValTyrAspCysSerLys	552
2131	TTTTGAcacaccctcaaagccgaactaaatcgaaccccaaagcaggaaaagcta PheSTP	554
2185	aaggaaccatcaaggcaaaatcgaaactaaaaaaaaaaatccaattaaaaaaaaacccc	
2245	tgagaatattcaccacaccagcgaaacagaatatccctccaaaattcagctcaccagcac	
2305	cagcacgaagaaaactctattttcttaaccgattaattcagagccacctccactttgcct	
2365	tgcttaataaacaacccgtaaaactgttttatacagagacagcaaaatcttggtttatt	
2425	aaaggacagtgttactccagataaacacgtaagtttcttcttgcttttcagagacctgctt	
2485	tcctctctccctctccctctcttgccttcttgcctctcactctcaactgtaagatatta	
2545	ttttatcctatgttgaagggaggggaaagtccccgtttatgaaagtcgctttcttttta	
2605	ttcatggacttgttttaaaatgtaaattgcaacatagtaattttatttttaatttgtagtt	
2665	ggatgtcgtggacaaacgccagaaagtgttccaaaacctgacgttaaattgacctgaaa	
2725	ctttaaatttgctttttttctcattataaaaagggaactgtattaatcttattctatc	
2785	ctcttttcttctttttgttgaacatatctattgtttgttttattaataaaattaccattca	
2845	qtttgaatgagacctatatgtctggatactttaatagagctttaattattacgaaaaaag	
2905	atttcagagataaaacactagaagttacctattctccacctaaatctctgaaaaatggag	
2965	aaacctctgactagtccatgtcaaattttactaaaagtctttttgtttagatttatttt	
3025	cctgcagcatctctcgaaaatgactatatagtcagcttgctttgaggctagtaaaaaag	
3085	atatttttctaaacagattggagttggcatataaaccaaatcagttttctcactaatgaca	
3145	gtccatgattcggaaattttaagcccatgaatcagccgcggtcttaccacggtgatgcct	
3205	gtgtgccgagagatgggactgtgcggccagatatgcacagataaatatttggttggtgta	
3265	ttccataataaattgcagtgcatataatacactcctgtgagccagatgttgaatagattt	
3325	tttctattatttcagtcctttataaaaggaaaaataaacagcatttttaattgtatgtat	
3385	ataattctccccattttacaatccttcatgtattacatagaaggattgcttttttaaaaa	
3445	tatactgcggttggaaggatatttaattctttgagaaactattttagaaaaatagtgtt	
3505	gtagaacaattatttttgaaaaagatttaaagcaataacaagaagggaagggcagaggagc	
3565	agaacatttttggtctagggtggtttcttttaaacattttttcttgtaattttacagtt	
3625	aaacctaggggacaatccggatttggccctcccccttttggtaaatcaaccaggaaatgtaa	
3685	taaatcattattcttagggtgatctgccctgccaatcagactttggggagatggcgattt	
3745	gattacagacgttcgggggggtggggggcttgagtttgggtttggagataatacagtttc	
3805	ctgctatctgcgcctcctatatagaggcaacacttaagcagtaattgctgttgcttggtg	
3865	tcaaaatttgatcattgtttaaggattgctgcaataataacactttaatttcagtcaaa	
3925	aaaaaaaaaaaaaaaaaaaaa	

Fig. 1B

Forkhead SYTHA.....S.....N.TRM.L.SE.....L.....Q.Q.R.....S.F.D...I...TPD.....F..HL..G.....CY...QK...CDK
 FKHL7 PKDMVKPPSYIALITMAIQNAPDKKITLNGIYQFIMDRFPFYRNKQGWQNSIRHNLSLNDCFTVKVPRDDKKPGKGYWTLPDPSYMFENGSLRRRRFFKKKD
 Mutations S M L

FKHL14 ...L.....E.....E.....
 FKHL18 TTEPT.....A...SS.GQRA.S..RV.G.A..H.RP.....R.....CHD..H.....TRQT
 FKHL11 AETPQ.....A...D.EQRY.....H.R.....D.....EKGR.....RCLD...NYR..K.KP.PGP
 FKHL12 .IQG.....A.LAH.GRRL.AA.R.TE.A...SPRK.....T.D...EPGN...N....AAAD.D...P..K..RAE
 FKHL15 .IQG.....A..AH.ERRL.G..K.TE.....PKK.....T.D..L.I.EAGR...N.A..NAED..S.....K..RS.
 FKHL9 ARQPA..S.....IQS.H.RL.S.CA.S...Y.RKP.....D...I.EPR...N.S..A.QD.D.....K.QRNQ
 FKHL8 RTRL.....IQS.K.RL.SE.CE.SG..Y.EKPA.....D...I.EPGN...N....E.AD.D.....K..RQP
 FKHL17 RSPL.....IQS.KKRL.SE.CE.SG..Y.EKPA.....D...I.EPGN...N....E.AD.D.....K..RQP
 FKHL5 IRRPE.....V...SS.T.RL.SE...IQS...F.GSY..K.V.....I.L.KGLGR...H..I.A.EF.....R...G.RR.C
 FKHL6 LRPE.....V...SS.S.RL.SE...LQA...F.GAY..K.V.....I.L.KGLGR...H..I.A.EF.....R...G.RR.C
 FKHL4 NGRYE..F.N..M..RQS.E.RL...E..KN.Y.E.....K.....HYDD...N.M..S.DDV.IG.TTGKL..STSP
 FKHL2 NGRYE..F.N..M..RQS.E.RL...E..KN.Y.E.....K.....HYDD...N.M..S.DDV.IG.TTGKL..STSP
 FKHL3 G.YEKP..F.N..M..RQS.E.RL...E..KN.Y.E.....H...D...K.....HYDD...N.M..S.DDV.IG.TTGKL..STSR
 FKHL10 LMKLYR.....S..A..HG...RL..SQ...YVA.N...NKS.A.....D.K.....EDD...
 FKHL13 TNDH.....AT..C..M.ASKAT...SA..KW.T.N.CYF.HADPT.....K..I...EKDE...GF.RI.QYAEKLLS.AFKK..LPFVHIH
 FKHR WGNLSYADLITK.IESS.EKRRLTISQ.YEMVTSVPPYFKDKGDSNSA..K.....HSK..IR.QNEGTSKSSWMNLNPEGKSGKSPRAASMD

Fig. 2

Clone Name	Image Number	Organism	Vector	Loc	5' Sequence	3' Sequence	Insert Size	Tissue	Contig
zr45a08	666326	Human		3'	AA232742	AA232201		NhHMPu	
zw04a06	768274	Human		3'		AA424787		NhHMPu	
zv90g12	767110	Human		3'	AA424381	AA424466		NhHMPu	
yw76b12	258143	Human	pT7T3D	3'	N40575			Placenta, 8 to 9 wk	
ze13t07	358885	Human		3'		W94629		Fetal Heart	
yw78d12	258359	Human		3'		N25875		Placenta, 8 to 9 wk	
zw05a06	768370	Human	pT7T3D	3'	AA495846		722	NhHMPu	
oj36t08	1500423	Human		3'		AA885880		NCI_CGAP_Lu5	
zd71b11	346077	Human		3'	W77980			Fetal Heart, 19 wk	
ah14c11	1156628	Human		3'		AA776534		Wilms Tumor	
oh48b09	1469849	Human		3'		AA865139		NCI_CGAP_GC4	
zd71b12	346079	Human		3'		W73917		Fetal Heart, 19 wk	
ze71a01	364392	Human	pT7T3D	3'	AA022618	AA022755	919	Fetal Heart, 19 wk	
ze13t07	358885	Human		3'	W94714			Fetal Heart, 19 wk	
ok90g07	1521276	Human		3'		AA902429		NCI_CGAP_Lu5	
yw78b12	258335	Human		3'		N25867		Placenta, 8 to 9 wk	
yw28c11	253556	Human	pBlue SK-	3'	H89575			Fetal Cochlea	
EST54452		Human		3'	AA348051			Fetal Heart	
EST38957		Human		3'	AA334694			Embryo, 9 wk	
yw30d03	253733	Human	pBlue SK-	3'	N75774	N22552	475	Fetal Cochlea	
nj57a04	996558	Human		3'	AA551599			NCI_CGAP_Pr9	
yw76d12	258167	Human	pT7T3D	3'	N40582			Placenta, 8 to 9 wk	
nv16g07	1220412	Human		3'		AA688135		NCI_CGAP_Pr22	
GEN-206f07		Human		3'	D56550			Aorta	
oj39104	1500703	Human		3'		AA886687		NCI_CGAP_Kid3	
GEN-288A05		Human		3'	D57248			Aorta	
vc30a07	776052	Mouse	pT7T3D	3'	AA276025			Kidney, 6 wk	
vu08t03	1180061	Mouse		5'	AA673797			Myotubes	
vw64c01	1248576	Mouse		3'	AA960591			Mammary Gland, 4 wk	
vg45c07	864300	Mouse	pT7T3D	3'		AA759405		Mammary Gland, 4 wk	
md53e12	372142	Mouse		3'		AA458089	936	Embryo, 13.5-14.5 dy	
mt72a07	419796	Mouse	pT7T3D	5'	W91182			Embryo, 13.5-14.5 dy	
vv53d11	1226133	Mouse	pT7T3D	5'	AA739434			Embryo, 13.5-14.5 dy	
me94t07	403237	Mouse	pT7T3D	3'				Thymus, 4 wk	
vc85b07		Mouse	pSPORT1	3'				Embryo, 13.5-14.5 dy	
mo83c06				3'				Embryo, 11.5 dy	
UI-R-AO-a1-b-03		Rat		3'	AA819240				
UI-R-E1-go-e-12		Rat		3'	AA964464			Embryo	

Fig. 3